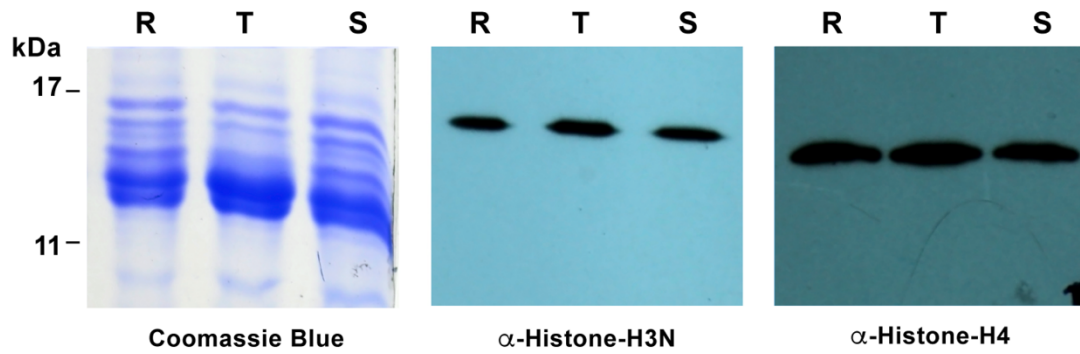


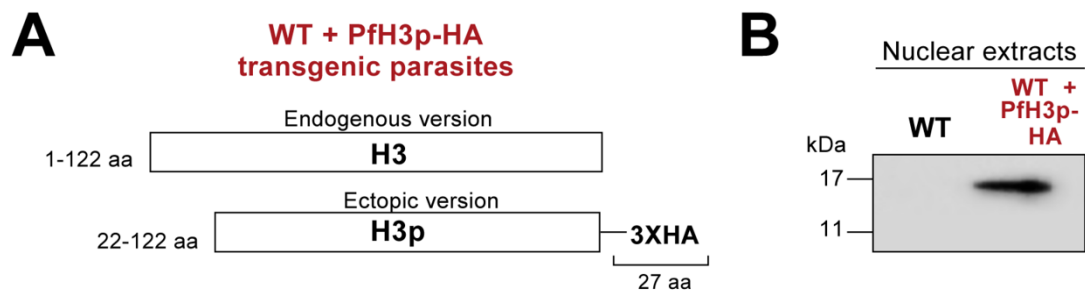
Appendix for Herrera-Solorio *et al*, 2018

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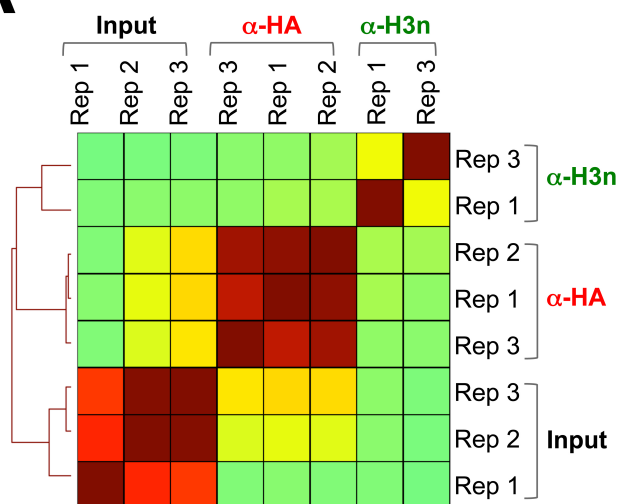


Appendix Figure S1: Mononucleosomes prepared from Ring (R), Trophozoite (T) and Schizont (S) stages of *P. falciparum* were separated on a denaturing polyacrylamide gel and visualized either by staining with Coomassie brilliant blue (C.B.) or by immunoblotting with anti-histone H3 N-terminal antibodies (α -Histone-H3n) or anti-Histone H4 antibodies. These data indicate that the clipping of Histone H3 occurs at the N-terminus.

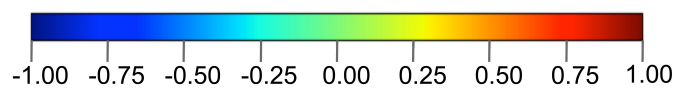
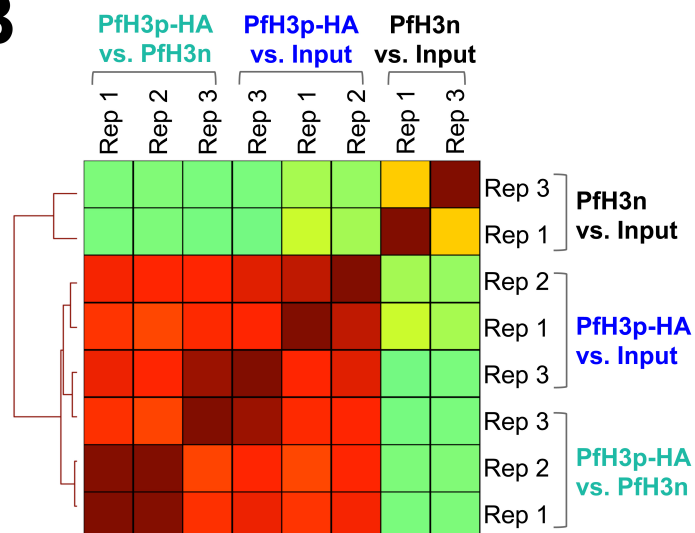


Appendix Figure S2: Ectopic expression of an HA-tagged version of clipped histone H3, PfH3p-HA (**A**), was confirmed in parasite nuclear extracts using immunoblotting with anti-HA antibodies (**B**).

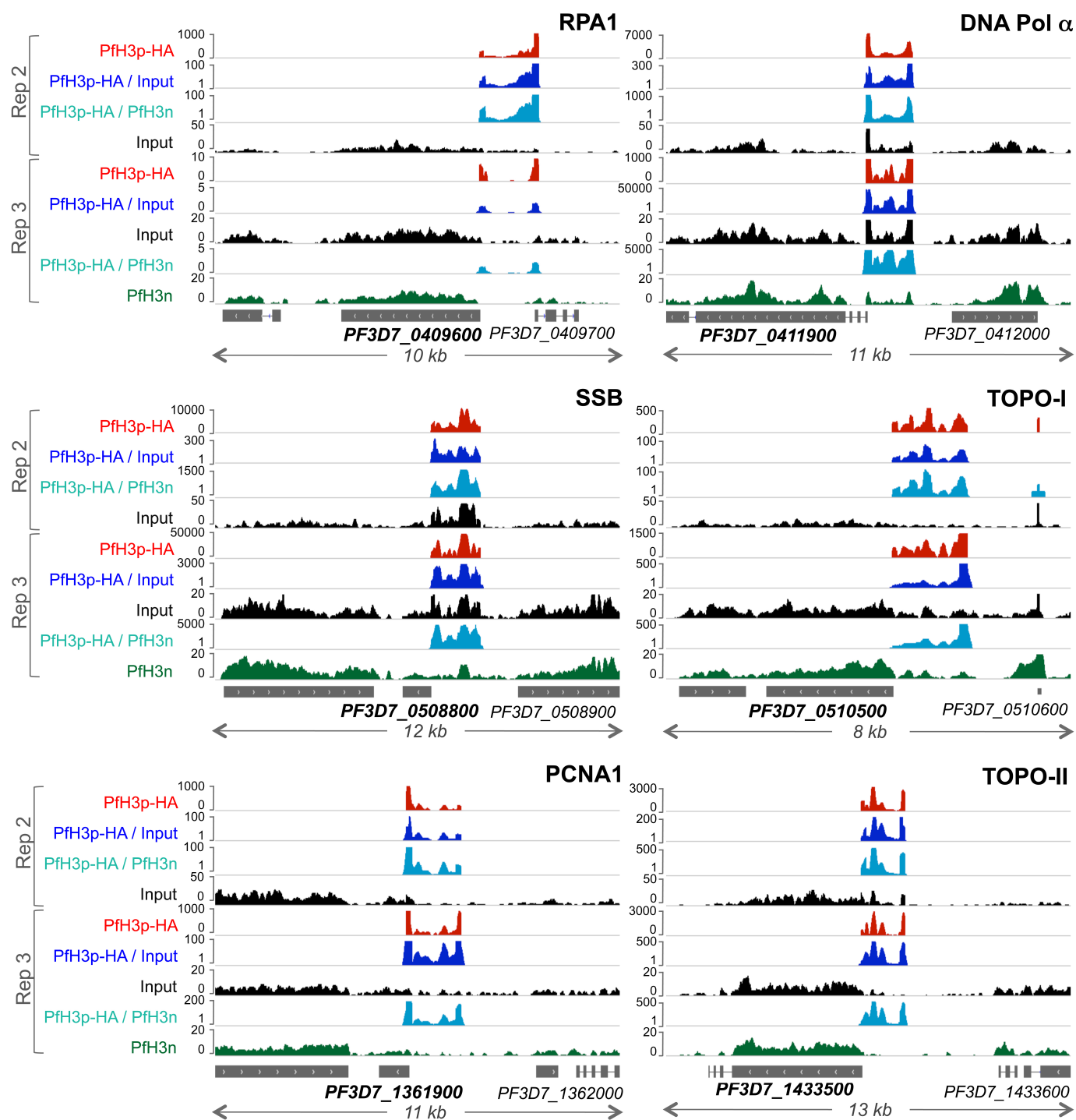
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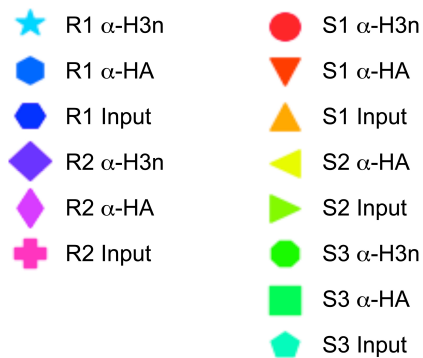
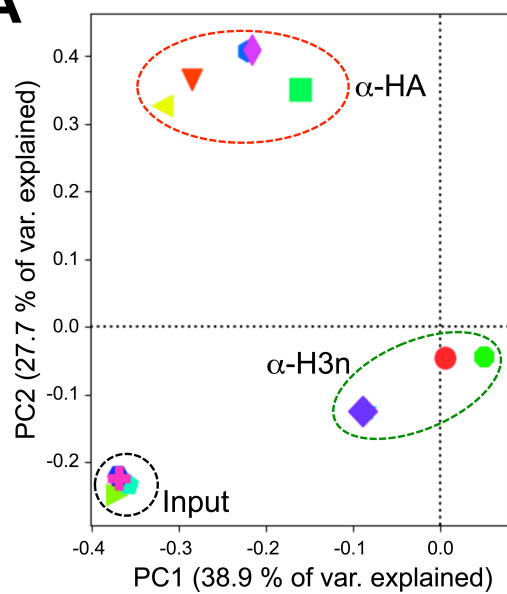
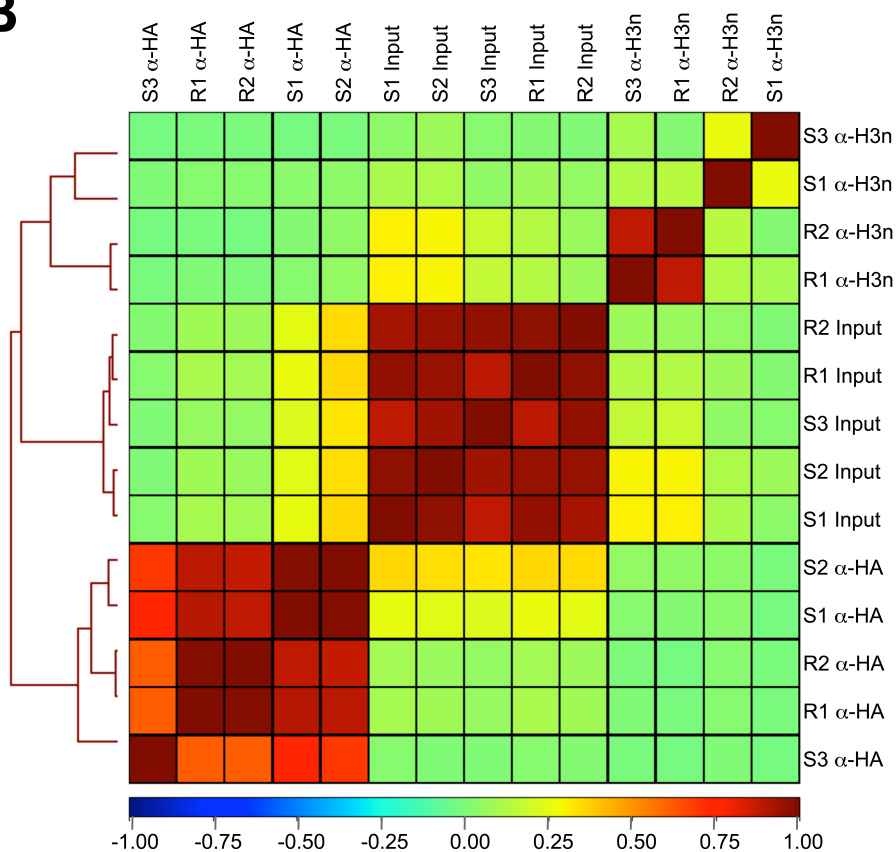
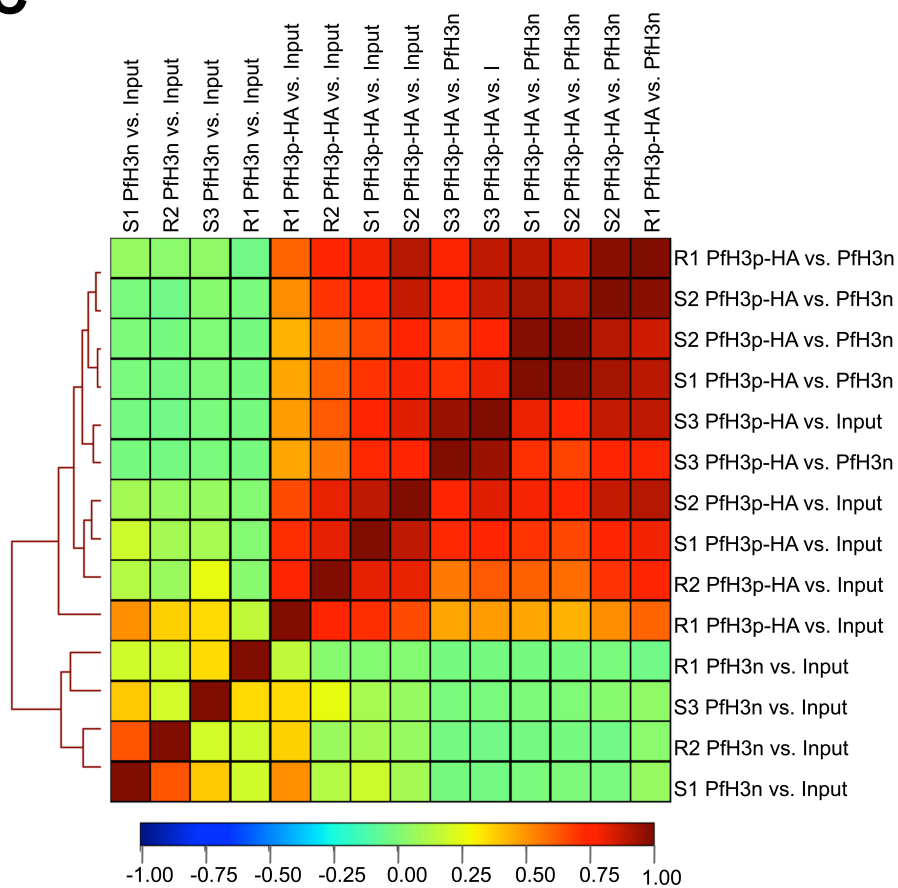
B



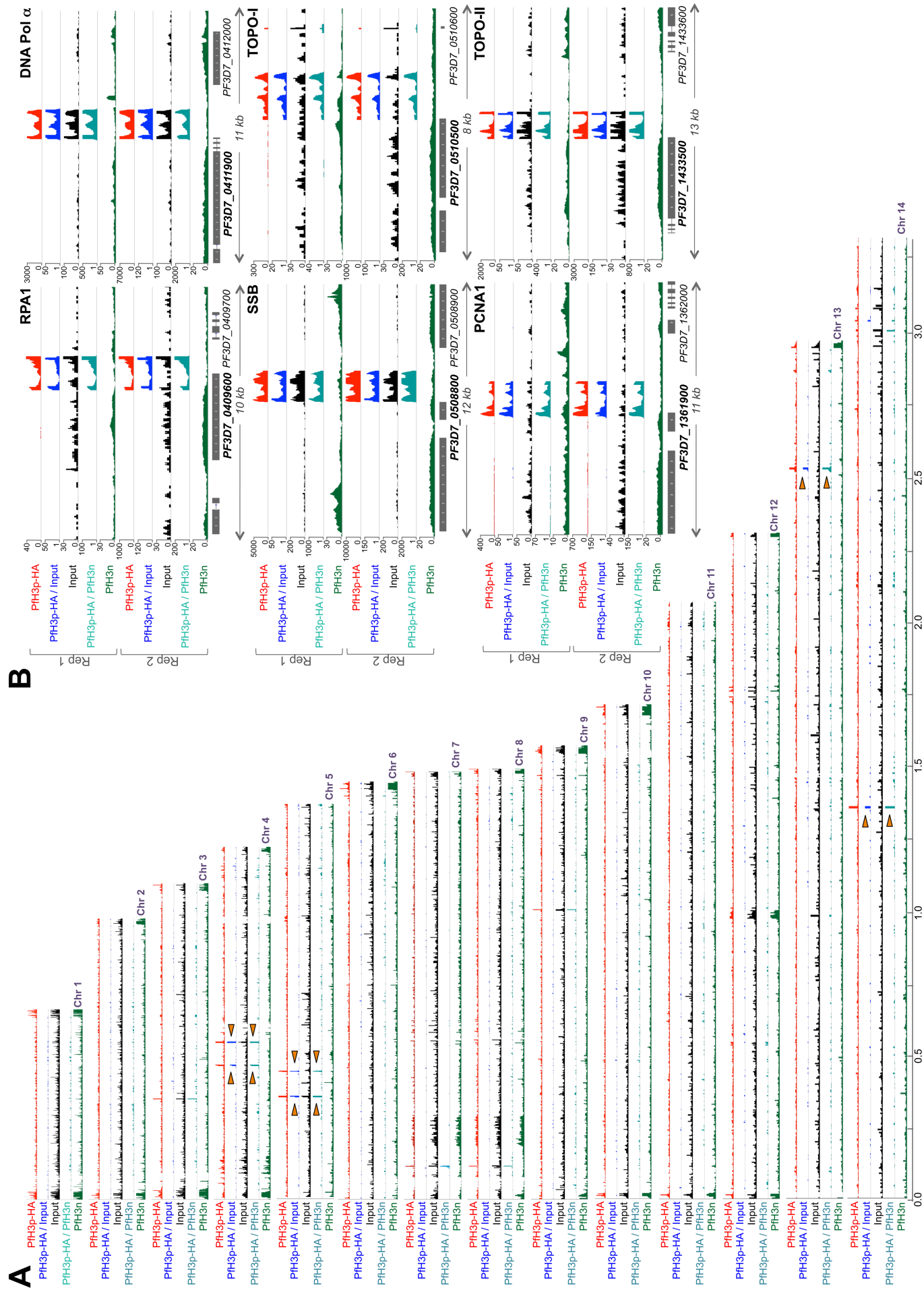
Appendix Figure S3: Correlations of **(A)** ChIP-seq bam files (genome-wide coverage normalized across 150 nt bins) and **(B)** fold enrichment of PfH3p-HA versus Input, PfH3p-HA versus PfH3n, or PfH3n versus Input comparisons for schizont stages (genome-wide coverage derived from MACS2, compared across contiguous 150 nt bins) were determined using a Pearson correlation analysis. The color scale indicates values of the Pearson correlation coefficient R from -1 to 1. Rep = Biological Replicate.



Appendix Figure S4: The genomic context of the six DNA replication genes enriched for PfH3p in schizont stages is shown for Biological Replicates 2 and 3. The fold enrichment of PfH3p-HA ChIP-seq signal over Input (PfH3p-HA / Input; blue) or PfH3n (PfH3p-HA / PfH3n; teal) is shown, as are the coverage plots of PfH3p-HA (red), PfH3n (green) and Input (black), which are represented as average reads per million over 1000 nt bins of the genome. DNA replication genes: Replication Protein A 1 (RPA1), Proliferating Cell Nuclear Antigen 1 (PCNA1), Single Stranded DNA binding protein (SSB), Topoisomerase I (TOPO-I), DNA polymerase alpha subunit (DNA pol a), and Topoisomerase II (TOPO-II) are highlighted and their directionality indicated.

A**B****C**

Appendix Figure S5: Correlations between Ring and Schizont stage PfH3p genome-wide localization. **A.** Principal Component Analysis of the different ChIP-seq replicates (bigwig files derived from deduplicated bam files) for ring (R; two replicates R1 and R2) and schizont (S; three replicates S1, S2 and S3) stage samples was performed using the plotPCA function of deepTools on a multibigwig summary file, over 150 nt bins. The Eigen values of the top two principal components PC1 and PC2 are shown and meaningful clustering of replicates based on treatment is highlighted. Rep = Biological Replicate. **B.** Correlations of ChIP-seq bam files (genome-wide coverage normalized across 150 nt bins) were determined using a Pearson Correlation Analysis. The color scale indicates values of the Pearson correlation coefficient R from -1 to 1. **C.** Correlation of fold enrichment (genome-wide coverage derived from MACS2, compared across contiguous 150 nt bins) of PfH3p-HA versus Input, PfH3p-HA versus PfH3n, or PfH3n versus Input comparisons for ring or schizont stages was determined using a Pearson correlation analysis. The color scale indicates values of the Pearson correlation coefficient R from -1 to 1. The data indicate that the PfH3p enrichment between ring and schizont stages is highly correlated, and hence conserved.



Appendix Figure S6: In *P. falciparum* Ring stages, ectopically expressed PfH3p is targeted to the 5' UTR of genes regulating DNA replication. **A.** Genome-wide distribution of ectopically expressed PfH3p-HA in *P. falciparum* ring stages is represented as fold-enrichment of PfH3p-HA ChIP-seq signal over Input (PfH3p-HA / Input in blue; y-axis scale 1-10) or over PfH3n (PfH3p-HA / Input in teal; y-axis scale 1-10) calculated using MACS2. The coverage of PfH3p-HA (red; y-axis scale 0-50), Input (black; y-axis scale 0-30) and PfH3n (green; y-axis scale 0-30) is also shown and represents average reads per million over 1000 nt bins of the genome. The x-axis represents chromosome size in Mb. Major MACS2-derived peaks identified in all replicates are indicated using an orange arrowhead. Note that the data correspond to Biological Replicate 1. **B.** The genomic context of the six peaks identified in both PfH3p-HA ChIP-seq replicates for Ring stages is shown. The fold enrichment of PfH3p-HA ChIP-seq signal over Input (PfH3p-HA / Input; blue) or PfH3n (PfH3p-HA / PfH3n; teal) is shown, as are the coverage plots of PfH3p-HA (red), PfH3n (green) and Input (black), which are represented as average reads per million over 1000 nt bins of the genome. DNA replication genes: Replication Protein A 1 (RPA1), Proliferating Cell Nuclear Antigen 1 (PCNA1), Single Stranded DNA binding protein (SSB), Topoisomerase I (TOPO-I), DNA polymerase alpha subunit (DNA pol a), and Topoisomerase II (TOPO-II) are highlighted and their directionality indicated. Rep = Biological Replicate.